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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,254

DATE: 07/16/2002 8-6  
TIME: 14:01:35

Input Set : A:\Sequence Listing 1321.2.29.1.txt

Output Set: N:\CRF3\07162002\J009254.raw

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3 <110> APPLICANT: University of Utah Research Foundation
4      Adderson, Elisabeth
5      Bohnsack, John
7 <120> TITLE OF INVENTION: Isolated Genes for Virulent Group B Streptococcus agalactiae
9 <130> FILE REFERENCE: 1321.2.29
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/009,254
C--> 11 <141> CURRENT FILING DATE: 2001-12-10
11 <150> PRIOR APPLICATION NUMBER: 60/140,084
12 <151> PRIOR FILING DATE: 1999-06-21
14 <160> NUMBER OF SEQ ID NOS: 10
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1509
20 <212> TYPE: DNA
21 <213> ORGANISM: Streptococcus agalactiae
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1509)
27 <400> SEQUENCE: 1
28 atg aaa aag aaa atg att caa tcg ctg tta gtg gcg agt tta gca ttt      48
29 Met Lys Lys Lys Met Ile Gln Ser Leu Leu Val Ala Ser Leu Ala Phe
30 1      5      10      15
32 ggt atg gct gta tca cca gtt acg ccg ata gct ttt gcc gct gag aca      96
33 Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr
34      20      25      30
36 ggg aca att aca gtt caa gat act caa aaa ggc gca acc tat aaa gca      144
37 Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
38      35      40      45
40 tat aaa gtt ttt gat gca gaa ata gat aat gca aat gta tct gat tcg      192
41 Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
42      50      55      60
44 aat aaa gat gga gct tct tat tta att cct caa ggt aaa gaa gct gag      240
45 Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
46 65      70      75      80
48 tat aaa gct tca act gat ttt aat tct ctt ttt acg aca act act aat      288
49 Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Asn
50      85      90      95
52 gga ggg aga aca tat gta act aaa aaa gat act gcg tca gca aat gag      336
53 Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
54      100      105      110
56 att gcg aca tgg gct aaa tct ata tca gct aat act aca cca gtt tcc      384
57 Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
58      115      120      125

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60 act gtt act gag tca aat aat gat ggt act gag gtt att aat gtt tcc      432
61 Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn Val Ser
62      130                      135                      140
64 caa tat gga tat tat tat gtt tct agc act gtt aat aat gga gct gta      480
65 Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
66 145                      150                      155                      160
68 att atg gtt aca tct gta act cca aat gct act att cat gaa aag aat      528
69 Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn
70      165                      170                      175
72 act gat gcg aca tgg gga gat ggt ggt gga aaa act gta gat caa aaa      576
73 Thr Asp Ala Thr Trp Gly Asp Gly Gly Lys Thr Val Asp Gln Lys
74      180                      185                      190
76 acg tac tcg gtt ggt gat aca gtc aaa tat act att act tat aag aat      624
77 Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
78      195                      200                      205
80 gca gtc aat tat cat ggt aca gaa aaa gtg tat caa tat gtt ata aag      672
81 Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys
82      210                      215                      220
84 gat act atg cca tct gct tct gta gtt gat ttg aac gaa ggg tct tat      720
85 Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
86 225                      230                      235                      240
88 gaa gta act att act gat gga tca ggg aat att aca act cta act caa      768
89 Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
90      245                      250                      255
92 ggt tcg gaa aaa gca act ggg aag tat aac ctg tta gag gaa aat aat      816
93 Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn
94      260                      265                      270
96 aat ttc acg att act att ccg tgg gca gct acc aat act cca acc gga      864
97 Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
98      275                      280                      285
100 aat act caa aat gga gct aat gat gac ttt ttt tat aag gga ata aat      912
101 Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
102      290                      295                      300
104 aca atc aca gtc act tat aca gga gta tta aag agt gga gct aaa cca      960
105 Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
106 305                      310                      315                      320
108 ggt tca gct gat tta cca gaa aat aca aac att gcg acc atc aac ccc      1008
109 Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
110      325                      330                      335
112 aat act agc aat gat gac cca ggt caa aaa gta aca gtg agg gat ggt      1056
113 Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly
114      340                      345                      350
116 caa att act ata aaa aaa att gat ggt tcc aca aaa gct tca tta caa      1104
117 Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
118      355                      360                      365
120 ggt gct ata ttt gtt tta aag aat gct acg ggt caa ttt cta aac ttt      1152
121 Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
122      370                      375                      380
124 aac gat aca aat aac gtt gaa tgg ggc aca gaa gct aat gca aca gaa      1200

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125 Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
126 385          390          395          400
128 tat aca aca gga gca gat ggt ata att acc att aca ggc ttg aaa gaa      1248
129 Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
130          405          410          415
132 ggt aca tac tat cta gtt gag aaa aag gct ccc tta ggt tac aat ttg      1296
133 Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
134          420          425          430
136 tta gat aac tct cag aag gtt att tta gga gat gga gcc act gat acg      1344
137 Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
138          435          440          445
140 act aat tca gat aac ctt tta gtt aac cca act gtt gaa aat aac aaa      1392
141 Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
142          450          455          460
144 ggt act gag ttg cct tca aca ggt ggt att ggt aca aca att ttc tac      1440
145 Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
146 465          470          475          480
148 att ata ggt gca att tta gta ata gga gca ggt atc gtg ctt gtt gct      1488
149 Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala
150          485          490          495
152 cgt cgt cgt tta cgt tct taa      1509
153 Arg Arg Arg Leu Arg Ser
154          500
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 502
159 <212> TYPE: PRT
160 <213> ORGANISM: Streptococcus agalactiae
162 <400> SEQUENCE: 2
164 Met Lys Lys Lys Met Ile Gln Ser Leu Leu Val Ala Ser Leu Ala Phe
165 1          5          10          15
168 Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr
169          20          25          30
172 Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
173          35          40          45
176 Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
177          50          55          60
180 Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
181 65          70          75          80
184 Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Thr Asn
185          85          90          95
188 Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
189          100          105          110
192 Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
193          115          120          125
196 Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn Val Ser
197          130          135          140
200 Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
201 145          150          155          160
204 Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn

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205          165          170          175
208 Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val Asp Gln Lys
209          180          185          190
212 Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
213          195          200          205
216 Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys
217          210          215          220
220 Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
221 225          230          235          240
224 Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
225          245          250          255
228 Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn
229          260          265          270
232 Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
233          275          280          285
236 Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
237          290          295          300
240 Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
241 305          310          315          320
244 Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
245          325          330          335
248 Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly
249          340          345          350
252 Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
253          355          360          365
256 Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
257          370          375          380
260 Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
261 385          390          395          400
264 Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
265          405          410          415
268 Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
269          420          425          430
272 Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
273          435          440          445
276 Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
277          450          455          460
280 Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
281 465          470          475          480
284 Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala
285          485          490          495
288 Arg Arg Arg Leu Arg Ser
289          500
292 <210> SEQ ID NO: 3
293 <211> LENGTH: 1692
294 <212> TYPE: DNA
295 <213> ORGANISM: Streptococcus agalactiae
297 <220> FEATURE:
298 <221> NAME/KEY: CDS

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## RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing 1321.2.29.1.txt

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299 <222> LOCATION: (1)..(1692)
301 <400> SEQUENCE: 3
302 att tgc att atg gtg atc gta ttc cgg att ata cag ata tta caa ggg      48
303 Ile Cys Ile Met Val Ile Val Phe Arg Ile Ile Gln Ile Leu Gln Gly
304 1          5          10          15
306 att ata tcc aag atc ctt cag gta cat att att ata agt atg att cac      96
307 Ile Ile Ser Lys Ile Leu Gln Val His Ile Ile Ile Ser Met Ile His
308          20          25          30
310 gag ata aag atc ccg act caa cta aag atg cct att ata cga cag ata      144
311 Glu Ile Lys Ile Pro Thr Gln Val Lys Met Pro Ile Ile Arg Gln Ile
312          35          40          45
314 cta gtc tca tca aat gtt gat aca aca act aag tac aag tac gta aaa      192
315 Leu Val Ser Ser Asn Val Asp Thr Thr Thr Lys Tyr Lys Tyr Val Lys
316          50          55          60
318 gac gct tac aaa tta gtc ggt tgg tat tat gtt aat cca tat ggt agt      240
319 Asp Ala Tyr Lys Leu Val Gly Trp Tyr Tyr Val Asn Pro Tyr Gly Ser
320 65          70          75          80
322 att aga cct tat aac ttt tca ggt gct gta act caa gat atc aat tta      288
323 Ile Arg Pro Tyr Asn Phe Ser Gly Ala Val Thr Gln Asp Ile Asn Leu
324          85          90          95
326 aga gct att tgg cga aag gct gga gat tat cat att ata tac agc aat      336
327 Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn
328          100          105          110
330 gat gct gtt ggt aca gat gga aag cca gca ttg gat gct tct ggt cag      384
331 Asp Ala Val Gly Thr Asp Gly Lys Pro Ala Leu Asp Ala Ser Gly Gln
332          115          120          125
334 caa tta caa aca agt aat gag cct act gac cct gat tcc tat gac gat      432
335 Gln Leu Gln Thr Ser Asn Glu Pro Thr Asp Pro Asp Ser Tyr Asp Asp
336          130          135          140
338 ggc tcc cat tca gcc tta ctg aga cgt ccg aca atg cca gat ggc tat      480
339 Gly Ser His Ser Ala Leu Leu Arg Arg Pro Thr Met Pro Asp Gly Tyr
340 145          150          155          160
342 cgt ttc cgt ggc tgg tgg tac aat ggt aaa att tat aac cca tat gat      528
343 Arg Phe Arg Gly Trp Trp Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp
344          165          170          175
346 tcc att gat att gac gcc cat tta gca gat gct aat aaa aat atc acc      576
347 Ser Ile Asp Ile Asp Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr
348          180          185          190
350 ata aaa cct gtc att att cca gta gga gat atc aaa tta gaa gat acc      624
351 Ile Lys Pro Val Ile Ile Pro Val Gly Asp Ile Lys Leu Glu Asp Thr
352          195          200          205
354 tcc atc aaa tac aat ggt aac ggt ggt act aga gta gaa aat ggt aat      672
355 Ser Ile Lys Tyr Asn Gly Asn Gly Gly Thr Arg Val Glu Asn Gly Asn
356          210          215          220
358 gtg gta aca caa gtg gag aca ccg cgt atg gag ttg aat agc aca act      720
359 Val Val Thr Gln Val Thr Pro Arg Met Glu Leu Asn Ser Thr Thr
360 225          230          235          240
362 aca att cct gaa aac caa tac ttt aca agg aca ggt tac aac ctt att      768
363 Thr Ile Pro Glu Asn Gln Tyr Phe Thr Arg Thr Gly Tyr Asn Leu Ile

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\Sequence Listing 1321.2.29.1.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 3

VERIFICATION SUMMARY

DATE: 07/16/2002

PATENT APPLICATION: US/10/009,254

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Input Set : A:\Sequence Listing 1321.2.29.1.txt

Output Set: N:\CRF3\07162002\J009254.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:655 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9

L:662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0